

CRF Errors Corrected by the STIC Systems Branch

Serial Number: 09/939,408A

CRF Processing Date: 1/24/2002

Edited by: Ar

Verified by: Ar (STIC staff)

ENTERED

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☒ Other: Seq 21, 28 - moved bases and amino acids over to left

***Examiner:** The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95



OIPE

RAW SEQUENCE LISTING

DATE: 01/29/2002

PATENT APPLICATION: US/09/939,408A

TIME: 10:50:20

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\01292002\I939408A.raw

p5

3 <110> APPLICANT: Yoshida, Roberta
 4 Kootstra, Anna
 7 <120> TITLE OF INVENTION: Phenylalanine Ammonia Lyase Polypeptide and
 8 Polynucleotide Sequences and Methods of Obtaining and
 9 Using Same
 11 <130> FILE REFERENCE: 29479/500NSCA
 13 <140> CURRENT APPLICATION NUMBER: US 09/939,408A
 17 <141> CURRENT FILING DATE: 2001-08-24
 19 <150> PRIOR APPLICATION NUMBER: US 09/624,693
 22 <151> PRIOR FILING DATE: 2000-07-24
 23 <150> PRIOR APPLICATION NUMBER: PCT/US01/23270
 26 <151> PRIOR FILING DATE: 2001-07-24
 29 <160> NUMBER OF SEQ ID NOS: 30
 31 <170> SOFTWARE: PatentIn Ver. 2.0
 33 <210> SEQ ID NO: 1
 34 <211> LENGTH: 35
 35 <212> TYPE: DNA
 36 <213> ORGANISM: Artificial Sequence
 38 <220> FEATURE:
 39 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic
 40 primer OLI 61
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 43 gacggatcca ctatggcbcc btcsgtsgac tcgat 35
 46 <210> SEQ ID NO: 2
 47 <211> LENGTH: 33
 48 <212> TYPE: DNA
 49 <213> ORGANISM: Artificial Sequence
 51 <220> FEATURE:
 52 <221> NAME/KEY: modified_base
 53 <222> LOCATION: (13)
 54 <223> OTHER INFORMATION: n = (a or c or g or t/u) or (unknown or other)
 56 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 58 Primer OLI 63
 60 <400> SEQUENCE: 2
 61 gacgaattct tangccatca tcttsacsag gac 33
 65 <210> SEQ ID NO: 3
 66 <211> LENGTH: 36
 67 <212> TYPE: DNA
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 70 <220> FEATURE:
 71 <221> NAME/KEY: modified_base
 73 <222> LOCATION: (24, 25, 29, 30, 34, 35)
 74 <223> OTHER INFORMATION: n = i or inosine

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 86 <213> ORGANISM: Artificial Sequence
 88 <220> FEATURE:
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 90 Primer GSP2
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 96 <210> SEQ ID NO: 5
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 99 <213> ORGANISM: Artificial Sequence
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 102 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 103 Primer AUAP
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 106 ggccacgcgt cgactagtagtac 20
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 146 ggtcaaggac gacgagggca ttct 24

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173     atcgaattcc actctaacc gtcactagca ctcgcg      36
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178 <212> TYPE: DNA
179 <213> ORGANISM: Artificial Sequence
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182 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
183     Primer OLI 78
185 <400> SEQUENCE: 11
186     atcggatccc acgacacgac gtcgaaaagc tgggtct      36
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195 <221> NAME/KEY: CDS
196 <222> LOCATION: (37)..(2196)
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198 <221> NAME/KEY: modified_base
199 <222> LOCATION: (494)
200 <223> OTHER INFORMATION: Other information: y = t or c
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203 <221> NAME/KEY: unsure
204 <222> LOCATION: (493)..(495)
206 <223> OTHER INFORMATION: Other information: Xaa = Val or Ala
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210                                     Met Ala Pro Ser Leu Asp
211                                     1             5
213     tcg etc gcc acc acg etc gcc aac ggc ttt acc aac ggc tcg cac gcc      102
214     Ser Leu Ala Thr Thr Leu Ala Asn Gly Phe Thr Asn Gly Ser His Ala
215             10             15             20

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217	gct ccg acc aag tcg gct gcg gcc ccc act tcg gct ctc cgc cgc acg	150
218	Ala Pro Thr Lys Ser Ala Ala Gly Pro Thr Ser Ala Leu Arg Arg Thr	
219	25 30 35	
221	ccc gcc ctc gat gcc cac gcc gcg cac cag tcg cag ctc gag atc gtg	198
222	Pro Gly Leu Asp Gly His Ala Ala His Gln Ser Gln Leu Glu Ile Val	
223	40 45 50	
225	cag gag ctc ctc agc gac ccc acc gac gac gtc gtc gag ctc agc ggg	246
227	Gln Glu Leu Leu Ser Asp Pro Thr Asp Asp Val Val Glu Leu Ser Gly	
228	55 60 65 70	
230	tac agc ctc acc gtc cgt gac gtt gtc gcc gcc cgc aag ggg cgc	294
231	Tyr Ser Leu Thr Val Arg Asp Val Val Gly Ala Ala Arg Lys Gly Arg	
232	75 80 85	
234	agg gtc cgc gtc cag aac gac gac gag atc cgc gca cgc gtc gac aag	342
235	Arg Val Arg Val Gln Asn Asp Asp Glu Ile Arg Ala Arg Val Asp Lys	
236	90 95 100	
238	agc gtc gac ttc ctc aag gcc cag ctt cag aac tcg gtc tac gga gtc	390
239	Ser Val Asp Phe Leu Lys Ala Gln Leu Gln Asn Ser Val Tyr Gly Val	
240	105 110 115	
243	acc acg ggt ttc ggt gcc tcg gcc gac acg agg act gag gat gca gtc	438
244	Thr Thr Gly Phe Gly Gly Ser Ala Asp Thr Arg Thr Glu Asp Ala Val	
245	120 125 130	
247	agc ctc cag aag gcg ctc atc gag cac cag ctc tgc gcc gtg acg ccg	486
248	Ser Leu Gln Lys Ala Leu Ile Glu His Gln Leu Cys Gly Val Thr Pro	
249	135 140 145 150	
251	acg tcc gyc tcg tcc ttc agc gtc gga cgc gcc ctc gag aac acg ctt	534
252	Thr Ser Xaa Ser Ser Phe Ser Val Gly Arg Gly Leu Glu Asn Thr Leu	
253	155 160 165	
255	ccg ctc gag gtc gtc cgc gcc gcc atg gtc atc cgc gtc aac tcg ctc	582
256	Pro Leu Glu Val Val Arg Gly Ala Met Val Ile Arg Val Asn Ser Leu	
257	170 175 180	
259	acg cgt gcc cac tcg gcc gtc cgc ctc gtc gtc ctt gag gcg ctc acc	630
260	Thr Arg Gly His Ser Ala Val Arg Leu Val Val Leu Glu Ala Leu Thr	
261	185 190 195	
263	aac ttc ttg aac cac cgc atc acg ccc atc gtc ccc ctc cgc gcc tcc	678
264	Asn Phe Leu Asn His Arg Ile Thr Pro Ile Val Pro Leu Arg Gly Ser	
265	200 205 210	
267	atc tcg gcg tcg gcc gac ctc agc ccg ctc tcg tac atc gcc gcc gcc	726
268	Ile Ser Ala Ser Gly Asp Leu Ser Pro Leu Ser Tyr Ile Ala Gly Ala	
269	215 220 225 230	
271	atc acc ggt cac ccc gac gtc aag gtt cac gtt ttg cac gag gga acc	774
272	Ile Thr Gly His Pro Asp Val Lys Val His Val Leu His Glu Gly Thr	
273	235 240 245	
275	gag aag atc atg ttt gcg cgc gag gcc atc tcg ctc ttt ggt ctc gag	822
276	Glu Lys Ile Met Phe Ala Arg Glu Ala Ile Ser Leu Phe Gly Leu Glu	
277	250 255 260	
279	gca gtc gtc ctc gcc ccg aag gag ggt ctc ggt ctg gtc aac gga acg	870
280	Ala Val Val Leu Gly Pro Lys Glu Gly Leu Gly Leu Val Asn Gly Thr	
281	265 270 275	
283	gcc gtc tcc gcc tcg atg gcg acc ctc agt ctg cac gac tcg cac atg	918

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284	Ala	Val	Ser	Ala	Ser	Met	Ala	Thr	Leu	Ser	Leu	His	Asp	Ser	His	Met	
285		280					285					290					
287	ctc	tcg	ctc	ctc	tcg	cag	gcc	ttg	acg	gct	ctc	acg	gtg	gag	gcc	atg	966
288	Leu	Ser	Leu	Leu	Ser	Gln	Ala	Leu	Thr	Ala	Leu	Thr	Val	Glu	Ala	Met	
289	295					300					305				310		
291	gtc	ggc	cag	cag	ggc	tcg	ttc	gcg	ccg	ttc	atc	cac	gac	gtc	tgc	cgc	1014
292	Val	Gly	Gln	Gln	Gly	Ser	Phe	Ala	Pro	Phe	Ile	His	Asp	Val	Cys	Arg	
293					315					320					325		
295	ccg	cac	ccc	ggc	cag	gtc	gag	gtc	gcg	cgc	aac	atc	cgc	acg	ctc	ctt	1062
297	Pro	His	Pro	Gly	Gln	Val	Glu	Val	Ala	Arg	Asn	Ile	Arg	Thr	Leu	Leu	
298				330				335					340				
300	tcc	ggc	tcg	tcg	ttt	gcc	gtt	gag	cac	gag	gag	gag	gtc	aag	gtc	aag	1110
301	Ser	Gly	Ser	Ser	Phe	Ala	Val	Glu	His	Glu	Glu	Glu	Val	Lys	Val	Lys	
302				345				350					355				
304	gac	gac	gag	ggc	att	ctt	cgc	cag	gac	cgc	tac	ccg	ctc	cgc	acg	tcg	1158
305	Asp	Asp	Glu	Gly	Ile	Leu	Arg	Gln	Asp	Arg	Tyr	Pro	Leu	Arg	Thr	Ser	
306		360				365					370						
308	cct	cag	ttc	ctc	ggc	ccg	ctc	gtg	gag	gac	atg	atg	cac	gcc	tac	tcg	1206
309	Pro	Gln	Phe	Leu	Gly	Pro	Leu	Val	Glu	Asp	Met	Met	His	Ala	Tyr	Ser	
310	375				380					385					390		
312	act	ctc	tcg	ctc	gag	aac	aac	acg	acg	acc	gac	aac	ccg	ctc	ctc	gac	1254
314	Thr	Leu	Ser	Leu	Glu	Asn	Asn	Thr	Thr	Thr	Asp	Asn	Pro	Leu	Leu	Asp	
315				395				400						405			
317	gtc	gag	aac	aag	cag	acc	gcg	cac	ggc	ggc	aac	ttc	cag	gcg	tcg	gct	1302
318	Val	Glu	Asn	Lys	Gln	Thr	Ala	His	Gly	Gly	Asn	Phe	Gln	Ala	Ser	Ala	
319				410				415					420				
321	gtc	tcg	att	tcg	atg	gag	aag	acc	agg	ctc	gca	ctc	gcc	ctc	atc	ggc	1350
322	Val	Ser	Ile	Ser	Met	Glu	Lys	Thr	Arg	Leu	Ala	Leu	Ala	Leu	Ile	Gly	
323				425				430					435				
325	aag	ctc	aac	ttc	acg	cag	tgc	acc	gag	ttg	ctc	aac	gct	gcc	atg	aac	1398
326	Lys	Leu	Asn	Phe	Thr	Gln	Cys	Thr	Glu	Leu	Leu	Asn	Ala	Ala	Met	Asn	
327		440				445					450						
329	cgc	ggc	ctg	cct	tcg	tgc	ctc	gct	gcc	gag	gac	ccg	tcg	ctc	aac	tat	1446
330	Arg	Gly	Leu	Pro	Ser	Cys	Leu	Ala	Ala	Glu	Asp	Pro	Ser	Leu	Asn	Tyr	
331	455				460					465				470			
333	cac	ggc	aag	ggc	ttg	gac	att	cac	atc	gct	gct	tac	gct	tcg	gag	ctc	1494
334	His	Gly	Lys	Gly	Leu	Asp	Ile	His	Ile	Ala	Ala	Tyr	Ala	Ser	Glu	Leu	
335				475				480					485				
337	ggc	cac	ctt	gcc	aac	ccg	gtc	act	acc	ttc	gtc	cag	ccc	gca	gag	atg	1542
338	Gly	His	Leu	Ala	Asn	Pro	Val	Thr	Thr	Phe	Val	Gln	Pro	Ala	Glu	Met	
339				490				495					500				
341	ggc	aac	cag	gcc	gtc	aac	tcg	ctc	gct	ctc	atc	tcc	gcg	cgc	cgc	act	1590
342	Gly	Asn	Gln	Ala	Val	Asn	Ser	Leu	Ala	Leu	Ile	Ser	Ala	Arg	Arg	Thr	
343		505				510					515						
345	gcc	gag	gcc	aac	gac	gtc	ctt	tct	ctc	ctt	ctc	gcc	tcg	cac	ctg	tac	1638
346	Ala	Glu	Ala	Asn	Asp	Val	Leu	Ser	Leu	Leu	Leu	Ala	Ser	His	Leu	Tyr	
347		520				525					530						
349	tgc	acg	ctc	cag	gcc	gtc	gac	ctc	cgc	gcg	atg	gag	ctc	gac	ttc	aag	1686
350	Cys	Thr	Leu	Gln	Ala	Val	Asp	Leu	Arg	Ala	Met	Glu	Leu	Asp	Phe	Lys	

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VERIFICATION SUMMARY

DATE: 01/29/2002

PATENT APPLICATION: US/09/939,408A

TIME: 10:50:21

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\01292002\I939408A.raw

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L:79 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:197 M:283 W: Missing Blank Line separator, <220> field identifier
L:252 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:416 M:283 W: Missing Blank Line separator, <400> field identifier
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DATE: 01/29/2002

PATENT APPLICATION: US/09/939,408A

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L:1908 M:283 W: Missing Blank Line separator, <220> field identifier
L:1910 M:283 W: Missing Blank Line separator, <400> field identifier
L:1915 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:27
L:1916 M:283 W: Missing Blank Line separator, <220> field identifier
L:1918 M:283 W: Missing Blank Line separator, <400> field identifier
L:1924 M:283 W: Missing Blank Line separator, <220> field identifier
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L:2150 M:283 W: Missing Blank Line separator, <220> field identifier
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L:2301 M:283 W: Missing Blank Line separator, <220> field identifier
L:2305 M:283 W: Missing Blank Line separator, <220> field identifier
L:2309 M:283 W: Missing Blank Line separator, <220> field identifier
L:2313 M:283 W: Missing Blank Line separator, <220> field identifier
L:2317 M:283 W: Missing Blank Line separator, <220> field identifier
L:2321 M:283 W: Missing Blank Line separator, <220> field identifier
L:2325 M:283 W: Missing Blank Line separator, <220> field identifier
L:2329 M:283 W: Missing Blank Line separator, <220> field identifier
L:2333 M:283 W: Missing Blank Line separator, <220> field identifier
L:2337 M:283 W: Missing Blank Line separator, <220> field identifier
L:2341 M:283 W: Missing Blank Line separator, <220> field identifier
L:2345 M:283 W: Missing Blank Line separator, <220> field identifier
L:2349 M:283 W: Missing Blank Line separator, <220> field identifier
L:2353 M:283 W: Missing Blank Line separator, <220> field identifier
L:2357 M:283 W: Missing Blank Line separator, <220> field identifier
L:2361 M:283 W: Missing Blank Line separator, <220> field identifier
L:2365 M:283 W: Missing Blank Line separator, <220> field identifier
L:2369 M:283 W: Missing Blank Line separator, <220> field identifier

VERIFICATION SUMMARY

DATE: 01/29/2002

PATENT APPLICATION: US/09/939,408A

TIME: 10:50:21

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\01292002\I939408A.raw

L:2373 M:283 W: Missing Blank Line separator, <220> field identifier
L:2377 M:283 W: Missing Blank Line separator, <220> field identifier
L:2381 M:283 W: Missing Blank Line separator, <220> field identifier
L:2385 M:283 W: Missing Blank Line separator, <220> field identifier
L:2389 M:283 W: Missing Blank Line separator, <220> field identifier
L:2393 M:283 W: Missing Blank Line separator, <220> field identifier